



SEQUENCE LISTING

<110> Bruce, Wesley B.

<120> A Nitrate-Responsive Root
Transcriptional Factor

<130> 1263

<140> US 09/970,624

<141> 2001-10-04

<150> US 60/238,292

<151> 2000-10-05

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1280

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (360)...(1082)

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tcctcccttg ggaaacctgc tgcctttgag ctttcttctt cgagagctcc caccagatct	180
cctcctcctt accttctttg gcacgttcgg cggcgcgcg gcgagaaagat agatcccgcc	240
atcgctgctg tcggtccttg cttccgatcg gagggccaca accacaacct ctcgctccat	300
agcgtgcaag cgcgagccag ggtcaagaag agagctagct agctataggc cggagatcg	359
atg ggg agg gga aag atc gtg atc cgc agg atc gat aac tcc acg agc	407
Met Gly Arg Gly Lys Ile Val Ile Arg Arg Ile Asp Asn Ser Thr Ser	
1 5 10 15	
cggtcag gtt acc ttc tcc aag cgc cgg aac ggg atc ttc aag aag gcc	455
Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala	
20 25 30	
aag gag ctc gcc atc ctc tgc gat gcg gag gtc ggc ctc gtc atc ttc	503
Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe	
35 40 45	
tcc agc acc ggc cgc ctc tac gag tac tct agc acc agc atg aaa tca	551
Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser	
50 55 60	
ggt ata gat cgg tac ggc aag gcc aag gaa gag cag caa gtc gtc gca	599
Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala	
65 70 75 80	
aat ccc aac tcg gag ctt aag ttt tgg caa agg gag gca gca agc ttg	647
Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu	

85	90	95	
aga caa caa ctg cac aac ttg caa gaa aat tat cgg cag ttg acg gga Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly 100 105 110			695
gat gat ctt tct ggg ctg aat gtc aaa gaa ctg cag tcc ctg gag aat Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn 115 120 125			743
caa ttg gaa aca agc ctg cgt ggt gtc cgc gca aag aag gac cat ctc Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu 130 135 140			791
ttg ata gat gag att cac gat ttg aat cga aag gca agt tta ttt cac Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His 145 150 155 160			839
caa gaa aat aca gac ttg tac aat aag atc aac ctg att cgc caa gaa Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu 165 170 175			887
aat gat gag tta cat aaa aag ata tat gag act gaa gga cca agt gga Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly 180 185 190			935
gtt aat cgg gag tca ccg act cca ttc aac ttt gca gta gta gaa acc Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr 195 200 205			983
aga gat gtt cct gtg caa ctt gaa ctc agc aca ctg cca cag caa aat Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn 210 215 220			1031
aac att gag cca tct act gct cct aag cta gga ttg caa tta att cca Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro 225 230 235 240			1079
tga agaagagtaa aactgccgtc ttatgatgct gaaggaaact atttattgtg *			1132
aagagatgat actcagagaa agacatatatt gtggcagggg gatttgagat atgaacttat aaatgtaatg caaataattt tcagaccgga atgggggtcgt ggaattcaga ggatgattgc tttctaaaaa aaaaaaaaaa aaaaaaaaaa			1192 1252 1280

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 <211> 240
 <212> PRT
 <213> Zea mays

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 Arg Gln Val Thr Phe Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala
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 Lys Glu Leu Ala Ile Leu Cys Asp Ala Glu Val Gly Leu Val Ile Phe
 35 40 45

Ser Ser Thr Gly Arg Leu Tyr Glu Tyr Ser Ser Thr Ser Met Lys Ser
 50 55 60
 Val Ile Asp Arg Tyr Gly Lys Ala Lys Glu Glu Gln Gln Val Val Ala
 65 70 75 80
 Asn Pro Asn Ser Glu Leu Lys Phe Trp Gln Arg Glu Ala Ala Ser Leu
 85 90 95
 Arg Gln Gln Leu His Asn Leu Gln Glu Asn Tyr Arg Gln Leu Thr Gly
 100 105 110
 Asp Asp Leu Ser Gly Leu Asn Val Lys Glu Leu Gln Ser Leu Glu Asn
 115 120 125
 Gln Leu Glu Thr Ser Leu Arg Gly Val Arg Ala Lys Lys Asp His Leu
 130 135 140
 Leu Ile Asp Glu Ile His Asp Leu Asn Arg Lys Ala Ser Leu Phe His
 145 150 155 160
 Gln Glu Asn Thr Asp Leu Tyr Asn Lys Ile Asn Leu Ile Arg Gln Glu
 165 170 175
 Asn Asp Glu Leu His Lys Lys Ile Tyr Glu Thr Glu Gly Pro Ser Gly
 180 185 190
 Val Asn Arg Glu Ser Pro Thr Pro Phe Asn Phe Ala Val Val Glu Thr
 195 200 205
 Arg Asp Val Pro Val Gln Leu Glu Leu Ser Thr Leu Pro Gln Gln Asn
 210 215 220
 Asn Ile Glu Pro Ser Thr Ala Pro Lys Leu Gly Leu Gln Leu Ile Pro
 225 230 235 240

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 <211> 36
 <212> DNA
 <213> Artificial Sequence

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36